RESULT 1

LOCUS   AW657531   549 bp   mRNA   EST   05-APR-2000
DEFINITION 110922 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION   AW657531

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	Query Match %	Length	DB ID	DB ID	Description
1		473.6	5.8	549	79	AW657531	AW657531 110922 MA
2		336.6	4.1	632	47	AL134888	AL134888 DKFZp762K
3		309.6	3.8	345	71	AW358862	AW358862 43799 MAR
4		302.6	3.7	341	72	AW416859	AW416859 52601 MAR
5	c	299.6	3.7	780	92	X83313	X83313 MMRS16REV M
6	c	285.4	3.5	538	119	AZ053598	AZ053598 RPCI-23-4
7	c	281.6	3.4	621	64	AW114058	AW114058 MC1153 mo
8	c	275	3.4	542	117	AQ929283	AQ929283 RPCI-23-2
9		275	3.3	602	117	AQ929513	AQ929513 RPCI-23-2
10	c	273.4	3.3	599	117	AQ919484	AQ919484 RPCI-23-2
11		273	3.3	704	69	AW215497	AW215497 up04n01.x
12		272	3.3	607	118	AZ015736	AZ015736 RPCI-23-3
13		271.6	3.3	542	119	AZ073478	AZ073478 RPCI-23-4
14		271	3.3	556	118	AQ998310	AQ998310 RPCI-23-3
15		270.8	3.3	691	117	AQ920012	AQ920012 RPCI-23-2
16		269.6	3.3	497	119	AZ060422	AZ060422 RPCI-23-4
17		265.8	3.2	535	119	AZ018423	AZ018423 RPCI-23-3
18		264.8	3.2	479	118	AQ988719	AQ988719 RPCI-23-3
19		262.8	3.2	580	119	AZ040659	AZ040659 RPCI-23-3
20		261.2	3.2	594	119	AZ024758	AZ024758 RPCI-23-3
21		259.2	3.2	564	118	AQ998182	AQ998182 RPCI-23-3
22		259.2	3.1	614	118	AQ994045	AQ994045 RPCI-23-3
23		258.4	3.1	510	40	AI506998	AI506998 v155g05.x
24		256.2	3.1	496	118	AZ003313	AZ003313 RPCI-23-2
25		255	3.1	590	119	AQ932217	AQ932217 RPCI-23-2
26		255	3.1	474	119	AZ019967	AZ019967 RPCI-23-2
27	c	251.8	3.1	626	119	AZ040324	AZ040324 RPCI-23-3
28		251.2	3.1	581	118	AZ006626	AZ006626 RPCI-23-3
29		249	3.0	671	118	AZ006294	AZ006294 RPCI-23-4
30		245	3.0	519	119	AZ073828	AZ073828 RPCI-23-4
31		244	3.0	620	117	AQ929961	AQ929961 RPCI-23-2
32		242	2.9	593	119	AZ024838	AZ024838 RPCI-23-3
33		241.8	2.9	560	119	AZ023929	AZ023929 RPCI-23-3
34		241.2	2.9	557	119	AZ060989	AZ060989 RPCI-23-4
35	c	241	2.9	766	42	AI648716	AI648716 uk28a08.x
36		239.4	2.9	503	117	AQ932220	AQ932220 RPCI-23-2
37		239	2.9	580	29	AA624937	AA624937 vn91d11.r
38		238.8	2.9	512	118	AQ993385	AQ993385 RPCI-23-2
39		238.6	2.9	610	119	AZ068000	AZ068000 RPCI-23-4
40		238	2.9	559	41	AI585993	AI585993 vs36g05.x
41		237.4	2.9	430	119	AZ023851	AZ023851 RPCI-23-3
42		237.2	2.9	481	117	AQ925578	AQ925578 RPCI-23-2
43		237.2	2.9	568	81	C76668	C76668 C76668 Mous
44		237.2	2.9	849	114	AQ744486	AQ744486 HS_5508_A
45		236.4	2.9	568	118	AZ008963	AZ008963 RPCI-23-3

117: gb_gss13:*
118: gb_gss14:*
119: gb_gss15:*
120: gb_gss16:*
121: gb_gss17:*
122: gb_gss18:*
123: gb_gss19:*
124: em_gss13:*

VERSION   AW657531.1 GI:7423429
KEYWORDS   EST.
SOURCE   Bos taurus.
  ORGANISM Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1 (bases 1 to 549)
  AUTHORS   Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,
            Bennett,G.A., Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A. and
            Keele,J.W.
  TITLE   Design and use of four pooled tissue normalized cDNA libraries for
            EST discovery in cattle
  JOURNAL   Unpublished (2000)
COMMENT   On Oct 30, 1998 this sequence version replaced gi:3815947.
            Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt.trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR Primers
            FORWARD: AGGAAAACAGCATAGACCAT
            BACKWARD: GTTTTCCCAGTGACGAG
            Plate: 94 row: E column: 12
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES   Location/Qualifiers
     source   1..549
                     /organism="Bos taurus"
                     /db_xref="taxon:9913"
                     /clone_lib="MARC 1BOV"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
                     Library made from pooled tissue from lymph node, ovary,
                     fat, hypothalamus, and pituitary."
BASE COUNT   145 a   144 c   121 g   139 t
ORIGIN

ALIGNMENTS

Query Match   5.8;   Score 473.6; DB 79;   Length 549;
Best Local Similarity   92.7%;   Pred. No. 2.1e-122;
Matches 508; Conservative 0; Mismatches 39; Indels 1; Gaps 1;

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Qy  6483  ctcccacaggtgttcctgttaagacaggacaggagagagactctcagtctccatccaggaggagcttt  6542
          ||||| |||||||||||||||||||||||  ||||||||||||||||||| |||||||||||||||| ||
Db     2  CTCCCCCGGGTGTTCCTGTTAAGACAGGACAGGACAGAGACTCTTCAGTCTCATCCAGGAGGCTTT  61

Qy  6543  ccaagccatcaactccaccgaccccgatcgccacttcttcttgtggcttttgtctctatcctc  6602
          |||||||||||||||| ||||||||||| |||||||| ||||||||  |||||||||||||||
Db    62  CCAAGCCATCAACTCACCGACCCCGATCGCCAGTTCTTCTTGTTGGCTTTGTCTCTATCCTC  121

Qy  6603  agggcctcctattatgagggatggctaaagaaagaaaatttcaatgtgaccaaagagca  6662
          ||||||||| |||||||||||||||||| ||| ||| |||||| |||||||||||||||
Db   122  AGGGCCTCCTTATTATGAGGGAATGGCTAGAGAAAGGAAAATTCAATGTGACCAAAGAGCA  181

Qy  6663  tagaaatcaatgtacatggggggtccgaaataagcttaccctcactgaagttccgggaa  6722
          |||||||||||||||||||||||| |||||||||  |||||||||||||||| |||||||
Db   182  TAGAAATCAATGTACATGGGGGGTCCGAAATAAGCTCACCCTCACTGAAGTTTCCGGGAA  241

Qy  6723  ggggacatgtcattaggaaaagctcccccaatcccacaccacccttgctatagtgtggt  6782
          ||||||||  || ||||||| |||||||||||||||||  |||| ||||| |||| ||||
Db   242  GGGGACAATGCATAGGAAAAAGCTCCCCCAATCCCACAACACCTTTGCAATAGTCATATGGT  301

Qy  6783  ttatgagcaggcctcagaaaatcagtatttagtacctggttataacagtggtgggcatg  6842
          |||||||||||| ||||||||||||||| ||||||| ||||||||||  || |||||| |
Db   302  TTATGAGCAGGCCTTAGAAAAATCAGTATTTAGTACCTGGTTATAACTGATAGGTGGGCACG  361

Qy  6843  caatactggttaacccctgttccaccctcagtcttcaacaacaatccaaaagatttctg  6902
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Db  6843  ...
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US 09-1/1-353-3.rst

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Db    262 CAATACTGGGTTAACTCCCTGTGTTCTTCTACCACAGTCTTAACCAATCAAAGATTTCTG 421
          |||||||||||||| |||||||| | |||||||| |||||||| ||||||| ||| |||
Qy   6903 tgtcatggtccaaatcgtccccgagtgtactactccgtggaaggtgtcctgatga 6962
Db    422 TGTCATGGTGTCCAGCTGTCCCCTGGGTACACTACCAATCCTGAGGAAGTAGTCATCGATGA 481
          |||||||| ||||| ||||||||||| |||||| |||||| |||||||||| |||||
Qy   6963 atatgactaattcggtataacggaccaaaaaagagagaaccgtatccctt-accctagctgtaa 7021
          ||||||||| ||| ||||| ||||||||||||||||||| ||| ||||||| ||||||||
Db    482 GTATGACTATCGGCCTACCCGGCTCAAAAAGAGAGACGCCCGTTAACCCTAGCCGTTA 541
Qy   7022 tgctcgga 7029
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Db    542 TACTAGGA 549
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RESULT 2

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LOCUS       AL134888    632 bp    mRNA        EST   25-FEB-2000
DEFINITION  DKFZp762K0910_r1 762 (synonym: hmel2) Homo sapiens cDNA clone
ACCESSION   AL134888
VERSION     AL134888.1  GI:6603075
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 632)
  AUTHORS   Blum,H., Bauersachs,S., Mewes,W., Weil,B. and Wiemann,S.
  TITLE     EST (Blum,H., Bauersachs,S., Mewes,H.W., Weil,B. and Wiemann,S.)
  JOURNAL   Unpublished (1999)
COMMENT     On Apr 7, 1998 this sequence version replaced gi:3034899.
            Contact: Blum H
            MIPS
            Am Klopferspitz 18a D-82152 Martinsried, Germany
            This is the 5' sequence of the clone insert.
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
            sequenced by LMU (Ludwig Maximilians University,
            Munich/Germany) within the cDNA sequencing consortium of the German
            Genome Project.
            No s1 sequence available.
            This clone (DKFZp762K0910) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES    Location/Qualifiers
     source 1..632
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="DKFZp762K0910"
            /clone_lib="762 (synonym: hmel2)"
            /tissue_type="melanoma (MeWo cell line)"
            /dev_stage="adult"
            /lab_host="DH10B"
            /note="Vector: pSport1; Site_1: NotI; Site_2: SalI"
BASE COUNT  162 a    195 c    143 g    132 t
ORIGIN
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Query Match   4.1%; Score 336.6; DB 47; Length 632;
Best Local Similarity 70.8%; Pred. No. 1.1e-83;
Matches 447; Conservative 0; Mismatches 184; Indels 0; Gaps 0;

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Qy   2605 cccaagcctggcagaaaccgcaggaggatgggtttggcaaagcaagttccccacagtta 2664
          ||||| |||||||||||| |||||||||||| ||||| |||||||||||||||| |||
Db      1 CCCAGGCCTGGGCAGAAAACCGGGGCGCCATGGGACTCGGCACGTTCGCCAAGCGCCTGATTA 60
Qy   2665 ttcaactgaaggccagtgctacacagtatcagtcaagagtaccccttgagtagtagagg 2724
          ||||||||||| ||||||| || |||||||||| ||| ||||||||| |||| |||||
Db     61 TACTTCTAAAGCACACCTCCACCCTGTGTCCATCAAAACAGTACCCATGTCACACGGAAG 120
Qy   2725 ctcgagcaggaagttggccgcatgttcaaagaattaatccaacaggggcatcctcagttccty 2784
          || ||||| ||| |||||| |||||||||||||||| |||||||||||| |||||||||
Db    121 CCGAGACTGGGGACTCAAAGCCCCACATACAGAGAGACTGTTGGACCAGGGGAATAATTGGTACCTT 180
Qy   2785 tccaatccccttggaataactccctgctcacecggttaggaaagcctgggaccaaatgattatc 2844
          ||||| ||||||||| |||||||||||| || |||||| |||| ||||||| ||| |||||||
Db    181 GCCAGTCCCCTGGAACACACACCCCTGCTGCCCGTTAAGAAAACCAGGGGACTAATGATTACA 240
Qy   2845 gaccagtacaggacttgagagaggtcaataaaaaggtgtcagggacatacaccaacggtcc 2904
          ||||| ||||| |||||||| |||||| |||||||||| ||||| ||| ||||||||||
Db    241 GGCCTGTCCCAGGATCTGAGAGAAGTCAACAAGCAGGGGGGGAAGAATATCCACCACCGTGC 300
Qy   2905 cgaacccttataacctcttgagcgccctcccgccctgaacggaactggtacacagtatgg 2964
          | |||||||||||||||||| |||| ||||| ||||| |||||||| ||||| |||| |
Db    301 CCAATCCTTACAACCTCTTAACCTGTTAAGTGGCACTCCCCTCCGTGCCCACCAGTGGGTACACTGTTG 360
Qy   2965 acttaaaagatgcccttctttctgcctgagattacacccccactagccaacccactttttgct 3024
          | |||||||||| ||||| ||| |||||||| |||||| ||||||| |||| |||| |||
Db    361 ATTTAAAAGATGGCTTTTTCTCGCCTGAGACTGCACCCCACCCAGTGAGCCTCTCTTTGCCT 420
Qy   3025 tcggaatggagagatccaggtacgggaagaacccgggcagctcaacctggaccgactgccc 3084
          | ||| ||||||||||||| |||||||||||||||| ||||| ||||||||||||| |||
Db    421 TTGAGTGGAGAGAATCCAGAAATGGGAAATCTCTGGACAATTGACCTGGACCGACTCCCAC 480
Qy   3085 aagggtcaagaactcccccgaccatctttgacgagaggcctacacaggggacctggccaact 3144
          ||||| |||| |||||| ||||| ||||| |||||| ||| ||||| |||||||| ||||
Db    481 AGGGTTCAAAAACAGTCCACCCGTGTTTGATGAGGCATTGCACAGGACCTAGCAGACT 540
Qy   3145 tcaggatccaacaccctcaggtgacctcctccagtacgtggatgacctgcttctggtgcg 3204
          ||| ||||| |||||| |||||| ||| |||||||||||| |||||| |||| |||||||
Db    541 TCCGGATCCAGCCACCCAGACTTGATCCTGCTACAGTAACGTGGACTACTGCTGTGGCCG 600
Qy   3205 gagccaccaaacaggagctgttagaaggtac 3235
          ||||| ||| |||||| ||||| ||| |||
Db    601 CTACTCCGGACTAGACTGCCAACAAGGTAC 631
```

RESULT 3

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LOCUS       AW358862    345 bp    mRNA        EST   04-FEB-2000
DEFINITION  43799 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION   AW358862
VERSION     AW358862.1  GI:6863512
KEYWORDS    EST.
SOURCE      pig.
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1 (bases 1 to 345)
  AUTHORS   Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
            Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A. and Keele,J.W.
  TITLE     EST discovery in swine
  JOURNAL   Unpublished (2000)
COMMENT     On Jul 9, 1999 this sequence version replaced gi:5866807.
            Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 20
            and -minmatch 12 options.
            PCR Primers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCACGTCACGACG
            Plate: 25  row: D  column: 18
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES    Location/Qualifiers
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            /db_xref="taxon:9823"
            /clone_lib="MARC 2PIG"
            /tissue_type="pooled"
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